BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT
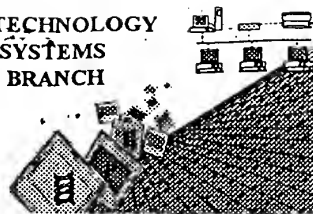
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/903,806B_

Source: _1600_

Date Processed by STIC: _4/10/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN ASSISTANCE: e-mail: robert.wax @ uspto.gov Telephone: 703-306-4119

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
          http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
   EFFECTIVE MAY 1, 2003 (via USPS): Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/01/2003

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/903,806 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _✓_ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

RAW SEQUENCE LISTING   DATE: 04/10/2003
PATENT APPLICATION: US/09/903,806B   TIME: 15:18:51

        Input Set : A:\P1618P2C3.txt
        Output Set: N:\CRF4\04102003\I903806B.raw

W-->   1 Patin Docket Preview *delete*
       7 <110> APPLICANT: Chen, Jian
       8   Goddard, Audrey
       9   Gurney, Austin L.
      10   Hillan, Kenneth   *Does No. Comply*
      11   Pennica, Diane   *Corrected Diskette Needed*
      12   Wood, William I.
      13   Yuan, Jean
      15 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
      16   Acids Encoding the Same
      18 <130> FILE REFERENCE: P1618P2C3
      20 <140> CURRENT APPLICATION NUMBER: US 09/903,806B
      21 <141> CURRENT FILING DATE: 2001-07-11
      23 <150> PRIOR APPLICATION NUMBER: US 09/665,350
      24 <151> PRIOR FILING DATE: 2000-09-18
      26 <150> PRIOR APPLICATION NUMBER: PCT/US00/04414
      27 <151> PRIOR FILING DATE: 2000-02-22   *Does Not Comply*
      29 <150> PRIOR APPLICATION NUMBER: PCT/US98/18824 *Corrected Diskette Needed*
      30 <151> PRIOR FILING DATE: 1998-09-10
      32 <150> PRIOR APPLICATION NUMBER: US 60/062,287
      33 <151> PRIOR FILING DATE: 1997-10-17   *pp 1-2*
      35 <160> NUMBER OF SEQ ID NOS: 424

ERRORED SEQUENCES

   15186 <210> SEQ ID NO: 424
   15187 <211> LENGTH: 17
   15188 <212> TYPE: PRT
   15189 <213> ORGANISM: Artificial sequence
   15191 <220> FEATURE:
   15192 <223> OTHER INFORMATION: Artificial polypeptide
   15194 <220> FEATURE:
W--> 15195 <221> NAME/KEY: Artificial Sequence   *Each location is an Xaa.*
   15196 <222> LOCATION: 1, 4, 6, 8, 10, 12, 14, 16   *This does not explain what Xaa's*
   15197 <223> OTHER INFORMATION: Artificial Sequence   *represent.*
   15199 <220> FEATURE:
   15200 <221> NAME/KEY: unsure
   15201 <222> LOCATION: 9, 11, 13, 15, 17   *Each location shows*
   15202 <223> OTHER INFORMATION: unknown amino acid?   *a clearly indicated amino acid*
   15204 <400> SEQUENCE: 424
E--> 15205   Xaa Asn Cys Xaa Cys Xaa ( ) Cys Xaa Cys Xaa Cys Xaa Gly Xaa
   15206   1   5   6   10 10   15

If the "." represents a gap,
the amino acids following the "."   *invalid*
need to be in a new sequence (new SEQ ID NO.) *Delete.*

misaligned amino acid nos. - see
Item 3 on Error Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,806B

DATE: 04/10/2003
TIME: 15:18:52

Input Set : A:\P1618P2C3.txt
Output Set: N:\CRF4\04102003\I903806B.raw

E--> 15208 Cys Xaa Asn

15

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence containing n or Xaa.

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence containing n or Xaa.

VERIFICATION SUMMARY   DATE: 04/10/2003
PATENT APPLICATION: US/09/903,806B-   TIME: 15:18:53

Input Set : A:\P1618P2C3.txt
Output Set: N:\CRF4\04102003\I903806B.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13 .
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:50
L:4499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113 after pos.:1450
L:5070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:1800
L:6720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174 after pos.:1650
L:6896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:525
L:8258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206 after pos.:950
M:341 Repeated in SeqNo=206
L:15195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:424
L:15205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:424 after pos.:0
L:15205 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:15205 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:341 Repeated in SeqNo=424
L:15208 M:252 E: No. of Seq. differs, <211> LENGTH:Input:17 Found:18 SEQ:424